

64851-02.ST25
SEQUENCE LISTING

<110> The Government of the United States of America, as represented by the Secretary of the Department of Health and Human Services
Flomerfelt, Francis
Gress, Ronald

<120> SPATIAL FOR ALTERING CELL PROLIFERATION

<130> 4239-64851-02

<150> PCT/US2003/036874

<151> 2003-11-18

<160> 7

<170> PatentIn version 3.3

<210> 1

<211> 933

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (84)..(677)

<223> Coding sequence

<400> 1

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gaaaccttgtt ttggaaccag ccc ctg ttt ctg ggg aat gta tat aag ggg agt 113
Leu Phe Leu Gly Asn Val Tyr Lys Gly Ser
1 5 10

tta gca cct cgt agg gat gag gtg act agt cca aag gca gag ccc cag 161
Leu Ala Pro Arg Arg Asp Glu Val Thr Ser Pro Lys Ala Glu Pro Gln
15 20 25

cca gag acg aag ccg gag aac ctt cca agg agc cac ggg gat gtt ggg 209
Pro Glu Thr Lys Pro Glu Asn Leu Pro Arg Ser His Gly Asp Val Gly
30 35 40

ctc cag aaa gag act gtg gtc cca ggc att gtg gat ttc gag ctg atc 257
Leu Gln Lys Glu Thr Val Val Pro Gly Ile Val Asp Phe Glu Leu Ile
45 50 55

cat gag gag ctg aag acc aca aag ccc caa aca tca caa cca aca ccc 305
His Glu Glu Leu Lys Thr Thr Lys Pro Gln Thr Ser Gln Pro Thr Pro
60 65 70

agt gcc tac cgc ttt gga cgc cta agc cac cat tcc ttc ttc tcg agg 353
Ser Ala Tyr Arg Phe Gly Arg Leu Ser His His Ser Phe Phe Ser Arg
75 80 85 90

cac cac ccc caa cca cag cga gtg act cat atc caa gat atc gct ggg 401
His His Pro Gln Pro Gln Arg Val Thr His Ile Gln Asp Ile Ala Gly

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95

100

105

aag cct gtc tgc gtg gtc agg gac gag ttc tct ctg tcg gcc ttg act 449
Lys Pro Val Cys Val Val Arg Asp Glu Phe Ser Leu Ser Ala Leu Thr
110 115 120

cag ccc aca ttc tta tcc cgc tgt ctg atg ggg atg ccc acc atc tct 497
Gln Pro Thr Phe Leu Ser Arg Cys Leu Met Gly Met Pro Thr Ile Ser
125 130 135

gtc ccc att ggg gat cca cag tcc aat cgg aac ccc cag ctt tct act 545
Val Pro Ile Gly Asp Pro Gln Ser Asn Arg Asn Pro Gln Leu Ser Thr
140 145 150

tct gac acc tgg agg aag aaa ctg aag gac ctg gct tcc cga gtg act 593
Ser Asp Thr Trp Arg Lys Lys Leu Lys Asp Leu Ala Ser Arg Val Thr
155 160 165 170

gtc ttc act aag gaa atc cag cca aag ccc gat gag gtt ggt gtt gca 641
Val Phe Thr Lys Glu Ile Gln Pro Lys Pro Asp Glu Val Gly Val Ala
175 180 185

caa aga atg gag cct aga aaa aaa agg cct tct taa gtctcccaa 687
Gln Arg Met Glu Pro Arg Lys Lys Arg Pro Ser
190 195

tgctcagctg ctggcacggg aggggaagga ccctcataac ctcgaaggta acagcgaaaa 747

tcaaagaaac acaaaatcac acctagcaga gaaatccaag aagggttccc agaaacaccc 807

tctaaagcaa ctgttccaa cctgtctaatt gccttgaccc ttgaatacag tttctcacac 867

tgcagtaacc cctgcccccg aaataaaatt atttcatta ctacttcaaa aaaaaaaaaa 927

aaaaaaaa 933

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<211> 197

<212> PRT

<213> Mus musculus

<400> 2

Leu Phe Leu Gly Asn Val Tyr Lys Gly Ser Leu Ala Pro Arg Arg Asp
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Glu Val Thr Ser Pro Lys Ala Glu Pro Gln Pro Glu Thr Lys Pro Glu
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Asn Leu Pro Arg Ser His Gly Asp Val Gly Leu Gln Lys Glu Thr Val
35 40 45

Val Pro Gly Ile Val Asp Phe Glu Leu Ile His Glu Glu Leu Lys Thr
50 55 60

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Thr Lys Pro Gln Thr Ser Gln Pro Thr Pro Ser Ala Tyr Arg Phe Gly
65 70 75 80

Arg Leu Ser His His Ser Phe Phe Ser Arg His His Pro Gln Pro Gln
85 90 95

Arg Val Thr His Ile Gln Asp Ile Ala Gly Lys Pro Val Cys Val Val
100 105 110

Arg Asp Glu Phe Ser Leu Ser Ala Leu Thr Gln Pro Thr Phe Leu Ser
115 120 125

Arg Cys Leu Met Gly Met Pro Thr Ile Ser Val Pro Ile Gly Asp Pro
130 135 140

Gln Ser Asn Arg Asn Pro Gln Leu Ser Thr Ser Asp Thr Trp Arg Lys
145 150 155 160

Lys Leu Lys Asp Leu Ala Ser Arg Val Thr Val Phe Thr Lys Glu Ile
165 170 175

Gln Pro Lys Pro Asp Glu Val Gly Val Ala Gln Arg Met Glu Pro Arg
180 185 190

Lys Lys Arg Pro Ser
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<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (84)..(779)
<223> Coding sequence

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gaaacttgtg ttggaaccag ccc ctg ttt ctg ggg aat gta tat aag ggg agt 113
Leu Phe Leu Gly Asn Val Tyr Lys Gly Ser
1 5 10

tta gca cct cgt agg gat gag gtg act agt cca aag gca gag ccc cag 161
Leu Ala Pro Arg Arg Asp Glu Val Thr Ser Pro Lys Ala Glu Pro Gln
15 20 25

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cca gag acg aag ccg gag aac ctt cca agg agc cac ggg gat gtt ggg	30	35	40	209
Pro Glu Thr Lys Pro Glu Asn Leu Pro Arg Ser His Gly Asp Val Gly				
ctc cag aaa gag act gtg gtc cca ggc att gtg gat ttc gag ctg atc	45	50	55	257
Leu Gln Lys Glu Thr Val Val Pro Gly Ile Val Asp Phe Glu Leu Ile				
cat gag gag ctg aag acc aca aag ccc caa aca tca caa cca aca ccc	60	65	70	305
His Glu Glu Leu Lys Thr Thr Lys Pro Gln Thr Ser Gln Pro Thr Pro				
agt gcc tac cgc ttt gga cgc cta agc cac cat tcc ttc ttc tcg agg	75	80	85	353
Ser Ala Tyr Arg Phe Gly Arg Leu Ser His His Ser Phe Phe Ser Arg				
cac cac ccc caa cca cag cga gtg act cat atc caa gtt aca gga aga	95	100	105	401
His His Pro Gln Pro Gln Arg Val Thr His Ile Gln Val Thr Gly Arg				
gag gac ctg gag cac tcc ctg ccc ctc acc acc tct ttc cag ctc ctt	110	115	120	449
Glu Asp Leu Glu His Ser Leu Pro Leu Thr Thr Ser Phe Gln Leu Leu				
caa gct cct ggg gtc cag ccc atg gat ctc act ccc tct gca gat atc	125	130	135	497
Gln Ala Pro Gly Val Gln Pro Met Asp Leu Thr Pro Ser Ala Asp Ile				
gct ggg aag cct gtc tgc gtg gtc agg gac gag ttc tct ctg tcg gcc	140	145	150	545
Ala Gly Lys Pro Val Cys Val Val Arg Asp Glu Phe Ser Leu Ser Ala				
ttg act cag ccc aca ttc tta tcc cgc tgt ctg atg ggg atg ccc acc	155	160	165	593
Leu Thr Gln Pro Thr Phe Leu Ser Arg Cys Leu Met Gly Met Pro Thr				
atc tct gtc ccc att ggg gat cca cag tcc aat cgg aac ccc cag ctt	175	180	185	641
Ile Ser Val Pro Ile Gly Asp Pro Gln Ser Asn Arg Asn Pro Gln Leu				
tct act tct gac acc tgg agg aag aaa ctg aag gac ctg gct tcc cga	190	195	200	689
Ser Thr Ser Asp Thr Trp Arg Lys Lys Leu Lys Asp Leu Ala Ser Arg				
gtg act gtc ttc act aag gaa atc cag cca aag ccc gat gag gtt ggt	205	210	215	737
Val Thr Val Phe Thr Lys Glu Ile Gln Pro Lys Pro Asp Glu Val Gly				
gtt gca caa aga atg gag cct aga aaa aaa agg cct tct taa	220	225	230	779
Val Ala Gln Arg Met Glu Pro Arg Lys Lys Arg Pro Ser				
gtctcccaa tgctcagctg ctggcacggg agggaaagga ccctcataac ctgcagg				839
acagcgaaaa tcaaagaaac acaaaatcac accttagcaga gaaatccaag aagggttccc				899
agaaaacaccc tctaaagcaa ctgttccaa cctgtctaat gccttgaccc ttgaatacag				959
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aaaaaaaaaa aaaaaaa

1035

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<211> 231
<212> PRT
<213> Mus musculus

<400> 4

Leu Phe Leu Gly Asn Val Tyr Lys Gly Ser Leu Ala Pro Arg Arg Asp
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Glu Val Thr Ser Pro Lys Ala Glu Pro Gln Pro Glu Thr Lys Pro Glu
20 25 30

Asn Leu Pro Arg Ser His Gly Asp Val Gly Leu Gln Lys Glu Thr Val
35 40 45

Val Pro Gly Ile Val Asp Phe Glu Leu Ile His Glu Glu Leu Lys Thr
50 55 60

Thr Lys Pro Gln Thr Ser Gln Pro Thr Pro Ser Ala Tyr Arg Phe Gly
65 70 75 80

Arg Leu Ser His His Ser Phe Phe Ser Arg His His Pro Gln Pro Gln
85 90 95

Arg Val Thr His Ile Gln Val Thr Gly Arg Glu Asp Leu Glu His Ser
100 105 110

Leu Pro Leu Thr Thr Ser Phe Gln Leu Leu Gln Ala Pro Gly Val Gln
115 120 125

Pro Met Asp Leu Thr Pro Ser Ala Asp Ile Ala Gly Lys Pro Val Cys
130 135 140

Val Val Arg Asp Glu Phe Ser Leu Ser Ala Leu Thr Gln Pro Thr Phe
145 150 155 160

Leu Ser Arg Cys Leu Met Gly Met Pro Thr Ile Ser Val Pro Ile Gly
165 170 175

Asp Pro Gln Ser Asn Arg Asn Pro Gln Leu Ser Thr Ser Asp Thr Trp
180 185 190

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Arg Lys Lys Leu Lys Asp Leu Ala Ser Arg Val Thr Val Phe Thr Lys
195 200 205

Glu Ile Gln Pro Lys Pro Asp Glu Val Gly Val Ala Gln Arg Met Glu
210 215 220

Pro Arg Lys Lys Arg Pro Ser
225 230

<210> 5
<211> 2117
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (40)..(1365)

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Met Ala Val Asp Gly
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ggg tgt ggg gac act gga gac tgg gaa ggt cgc tgg aac cat gta aag 102
Gly Cys Gly Asp Thr Gly Asp Trp Glu Gly Arg Trp Asn His Val Lys
10 15 20

aag ttc ctc gag cgg tct gga ccc ttc aca cac ccc gat ttc gaa cca 150
Lys Phe Leu Glu Arg Ser Gly Pro Phe Thr His Pro Asp Phe Glu Pro
25 30 35

agc act gaa tca ctc cag ttc ttg tta gat aca tgt aaa gtt cta gtc 198
Ser Thr Glu Ser Leu Gln Phe Leu Leu Asp Thr Cys Lys Val Leu Val
40 45 50

att gga gct ggt ggc tta gga tgt gag ctt ctg aaa aat ctg gca tta 246
Ile Gly Ala Gly Leu Gly Cys Glu Leu Leu Lys Asn Leu Ala Leu
55 60 65

tct ggt ttt aga cag att cat gtt ata gac atg gac act ata gat gtt 294
Ser Gly Phe Arg Gln Ile His Val Ile Asp Met Asp Thr Ile Asp Val
70 75 80 85

tcc aat tta aat aga cag ttt tta ttt agg cct aaa gat gty gga aga 342
Ser Asn Leu Asn Arg Gln Phe Leu Phe Arg Pro Lys Asp Xaa Gly Arg
90 95 100

ccc aag gct gaa gtt gct gca gaa ttc cta aat gac aga gtt cct aac 390
Pro Lys Ala Glu Val Ala Ala Glu Phe Leu Asn Asp Arg Val Pro Asn
105 110 115

tgc aac gtg gtm cca cat ttc aac aag atw caa gat ttt aac gac act 438
Cys Asn Val Xaa Pro His Phe Asn Lys Xaa Gln Asp Phe Asn Asp Thr
120 125 130

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ttc tac cga caa ttt cat atc att gta tgt ggc ctg gac tct atc ata Phe Tyr Arg Gln Phe His Ile Ile Val Cys Gly Leu Asp Ser Ile Ile 135 140 145	486
gcg aga aga tgg atc aat gga atg ctg ata tct ctt cta aat tat gaa Ala Arg Arg Trp Ile Asn Gly Met Leu Ile Ser Leu Leu Asn Tyr Glu 150 155 160 165	534
gat ggt gtg ttg gat cca agc tcc att gta cct ttg ata gat ggg ggg Asp Gly Val Leu Asp Pro Ser Ser Ile Val Pro Leu Ile Asp Gly Gly 170 175 180	582
aca gaa ggc ttt aaa ggg aat gcc cga gtg att ttg cct gga atg acc Thr Glu Gly Phe Lys Gly Asn Ala Arg Val Ile Leu Pro Gly Met Thr 185 190 195	630
gct tgt att gag tgc act ctg gaa ctt tac cca cca cag gtc aat ttc Ala Cys Ile Glu Cys Thr Leu Glu Leu Tyr Pro Pro Gln Val Asn Phe 200 205 210	678
ccc atg tgt acc att gca tct atg ccy agg ctc cca gaa cac tgt atc Pro Met Cys Thr Ile Ala Ser Met Xaa Arg Leu Pro Glu His Cys Ile 215 220 225	726
gag tat gtg agg atg ttg caa tgg cct aaa gag cag cct ttt gga gat Glu Tyr Val Arg Met Leu Gln Trp Pro Lys Glu Gln Pro Phe Gly Asp 230 235 240 245	774
ggg gtt cca tta gat gga gat gac cct gaa cat att cag tgg att ttc Gly Val Pro Leu Asp Gly Asp Pro Glu His Ile Gln Trp Ile Phe 250 255 260	822
caa aag tcc ata gag aga gca tca caa tat aat att aga ggc gtt acc Gln Lys Ser Ile Glu Arg Ala Ser Gln Tyr Asn Ile Arg Gly Val Thr 265 270 275	870
tac aga ctc act caa ggg gtg gta aaa cga atc att cct gca gta gct Tyr Arg Leu Thr Gln Gly Val Val Lys Arg Ile Ile Pro Ala Val Ala 280 285 290	918
tct aca aat gca gtc att gca gct gtg tgt gcc act gag gtt ttc aag Ser Thr Asn Ala Val Ile Ala Ala Val Cys Ala Thr Glu Val Phe Lys 295 300 305	966
ata gct aca agt gcg tac att ccc ctt aat aac tac ctg gta ttc aat Ile Ala Thr Ser Ala Tyr Ile Pro Leu Asn Asn Tyr Leu Val Phe Asn 310 315 320 325	1014
gat gta gat ggg ctg tac act tac acg ttt gaa gca gag aga aag gaa Asp Val Asp Gly Leu Tyr Thr Tyr Phe Glu Ala Glu Arg Lys Glu 330 335 340	1062
aac tgt cca gca tgt agc caa ctt cct caa aac att cag ttt tcc cca Asn Cys Pro Ala Cys Ser Gln Leu Pro Gln Asn Ile Gln Phe Ser Pro 345 350 355	1110
tca gct aaa cta cag gag gtc tta gac tac cta acc aac agt gct tct Ser Ala Lys Leu Gln Glu Val Leu Asp Tyr Leu Thr Asn Ser Ala Ser 360 365 370	1158

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ctg caa atg aag tct ccg gct atc aca gcc aca tta gag ggg aag aac	1206
Leu Gln Met Lys Ser Pro Ala Ile Thr Ala Thr Leu Glu Gly Lys Asn	
375 380 385	
agg aca ctt tac tta cag tca gta acg tct att gaa gaa cga acc agg	1254
Arg Thr Leu Tyr Leu Gln Ser Val Thr Ser Ile Glu Glu Arg Thr Arg	
390 395 400 405	
ccc aat ctt tcc aaa aca tta aaa gaa ctg gga cta gtt gat gga caa	1302
Pro Asn Leu Ser Lys Thr Leu Lys Glu Leu Gly Leu Val Asp Gly Gln	
410 415 420	
gaa ctg gct gtt gat gtc act aca cca cag act gta cta ttc aaa	1350
Glu Leu Ala Val Ala Asp Val Thr Thr Pro Gln Thr Val Leu Phe Lys	
425 430 435	
ctt cat ttt act taa ggaaaataaaa tctgcacata atagaaaatt catagaaaata	1405
Leu His Phe Thr	
440	
atataacttta taaatgatat gaaattgaag agccttgaag atgaggcaga ggggaacatc	1465
caagaaaagga aatttaattt gtgtcatttt tagcatttgcgtggctagaa tttgactttt	1525
atatatatac atatatataa aaaaggactg actctttttt aactttataa gtttctcttg	1585
aagactgaac tttggggtttggcttagcaag cattttcatt ttattactat ggaaagctat	1645
gccttcagga gagattatga acaagtgtgt tgcttcttta aagcaggaca aacactgtct	1705
tgtgtgtgag tttgttgtgg tcaaagagca tattcctcag cgtgtatctg aaatccacat	1765
gtgttagaaat gtctcctggg atggaaatga ggagctatgt ctgaagaata gtaaaatattc	1825
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aacagtatta tagattcata cctgtgcatttgcagaattttaa cttgtccatg ataatttgcata	2005
gcaatgccac agagaccagt atgcacaaat ttaaaccaag acatggctgt tcaaagaaaa	2065
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<210> 6
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 <212> PRT
 <213> Mus musculus

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 <222> (99)..(99)
 <223> The 'Xaa' at location 99 stands for Val.

<220>
 <221> misc_feature
 <222> (121)..(121)

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<223> The 'Xaa' at location 121 stands for Val.

<220>

<221> misc_feature

<222> (127)..(127)

<223> The 'Xaa' at location 127 stands for Ile.

<220>

<221> misc_feature

<222> (222)..(222)

<223> The 'Xaa' at location 222 stands for Pro.

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Trp Asn His Val Lys Lys Phe Leu Glu Arg Ser Gly Pro Phe Thr His
20 25 30

Pro Asp Phe Glu Pro Ser Thr Glu Ser Leu Gln Phe Leu Leu Asp Thr
35 40 45

Cys Lys Val Leu Val Ile Gly Ala Gly Gly Leu Gly Cys Glu Leu Leu
50 55 60

Lys Asn Leu Ala Leu Ser Gly Phe Arg Gln Ile His Val Ile Asp Met
65 70 75 80

Asp Thr Ile Asp Val Ser Asn Leu Asn Arg Gln Phe Leu Phe Arg Pro
85 90 95

Lys Asp Xaa Gly Arg Pro Lys Ala Glu Val Ala Ala Glu Phe Leu Asn
100 105 110

Asp Arg Val Pro Asn Cys Asn Val Xaa Pro His Phe Asn Lys Xaa Gln
115 120 125

Asp Phe Asn Asp Thr Phe Tyr Arg Gln Phe His Ile Ile Val Cys Gly
130 135 140

Leu Asp Ser Ile Ile Ala Arg Arg Trp Ile Asn Gly Met Leu Ile Ser
145 150 155 160

Leu Leu Asn Tyr Glu Asp Gly Val Leu Asp Pro Ser Ser Ile Val Pro
165 170 175

Leu Ile Asp Gly Gly Thr Glu Gly Phe Lys Gly Asn Ala Arg Val Ile

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180

185

190

Leu Pro Gly Met Thr Ala Cys Ile Glu Cys Thr Leu Glu Leu Tyr Pro
195 200 205

Pro Gln Val Asn Phe Pro Met Cys Thr Ile Ala Ser Met Xaa Arg Leu
210 215 220

Pro Glu His Cys Ile Glu Tyr Val Arg Met Leu Gln Trp Pro Lys Glu
225 230 235 240

Gln Pro Phe Gly Asp Gly Val Pro Leu Asp Gly Asp Asp Pro Glu His
245 250 255

Ile Gln Trp Ile Phe Gln Lys Ser Ile Glu Arg Ala Ser Gln Tyr Asn
260 265 270

Ile Arg Gly Val Thr Tyr Arg Leu Thr Gln Gly Val Val Lys Arg Ile
275 280 285

Ile Pro Ala Val Ala Ser Thr Asn Ala Val Ile Ala Ala Val Cys Ala
290 295 300

Thr Glu Val Phe Lys Ile Ala Thr Ser Ala Tyr Ile Pro Leu Asn Asn
305 310 315 320

Tyr Leu Val Phe Asn Asp Val Asp Gly Leu Tyr Thr Tyr Thr Phe Glu
325 330 335

Ala Glu Arg Lys Glu Asn Cys Pro Ala Cys Ser Gln Leu Pro Gln Asn
340 345 350

Ile Gln Phe Ser Pro Ser Ala Lys Leu Gln Glu Val Leu Asp Tyr Leu
355 360 365

Thr Asn Ser Ala Ser Leu Gln Met Lys Ser Pro Ala Ile Thr Ala Thr
370 375 380

Leu Glu Gly Lys Asn Arg Thr Leu Tyr Leu Gln Ser Val Thr Ser Ile
385 390 395 400

Glu Glu Arg Thr Arg Pro Asn Leu Ser Lys Thr Leu Lys Glu Leu Gly
405 410 415

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Leu Val Asp Gly Gln Glu Leu Ala Val Ala Asp Val Thr Thr Pro Gln
 420 425 430

Thr Val Leu Phe Lys Leu His Phe Thr
 435 440

<210> 7
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 tgttttgttt ttttgacacg agggttctgg aggttgaact catgccttca cgcttgcagg 1380

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gcaaacactt	tgca	gacgaa	gccatctccc	cagccccct	cttagagtat	ctccagcatg	1440		
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gaaataaata	gctccctcag	gactgatccc	aagaatcaa	gctcccaaag	gctcaactat		2160		
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ggc	ctatgtt	ctggagttgt	ggg	taac	cttagca	accactggc	tcagcat	2460	
cacaaagcaa	caggttgc	cacaattccg	aca	aggc	ctta	cc	ttgtt	2520	
ccatcttgg	caggcaccag	ggg	ctt	ctt	gtc	tct	ctgg	2580	
gat	ttcagg	cc	ctc	cagg	atgaaatgg	atc	tggtcc	aggtgaca	2640
aaaggaattt	tg	gggg	gata	agg	ttcc	tgt	gggtc	c	2700
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